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Fig. 13-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of "original" pig-baboon chimeric uricase ("PBC") vs. pig uricase

"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight:	50	Average Match:	10.000
Length Weight:	3	Average Mismatch:	-9.000
Quality:	8770	Length:	915
Ratio:	9.585	Gaps:	0
Percent Similarity:	97.814	Percent Identity:	97.814

Match display thresholds for the alignment(s):

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| = IDENTITY
: = 5
. = 1

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PBC.seq x pig.seq July 25, 1998 08:10 ..

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PBC   1  ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT  50
      |||
PIG   1  ATGGCTCATTACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTTGT  50
      |||
      51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG  100
      |||
      51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG  100
      |||
     101  ATGGAATAATACACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT  150
      |||
     101  ATGGAATAATACACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT  150
      |||
     151  TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC  200
      |||
     151  TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAGATGTCATCCC  200
      |||
     201  TACAGACACCATCAAGAACACAGTTAATGTCTCTGGCGAAGTTCAAAGGCA  250
      |||
     201  TACAGACACCATCAAGAACACAGTTAATGTCTCTGGCGAAGTTCAAAGGCA  250
      |||
     251  TCAAAAGCATAGAAAACTTTGTCTGTGACTATCTGTGAGCATTTCCTTTCT  300
      |||
     251  TCAAAAGCATAGAAAACTTTGTCTGTGACTATCTGTGAGCATTTCCTTTCT  300
      |||
     301  TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCCTTG  350
      |||
     301  TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCCTTG  350
      |||
     351  GAAGCGTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTATTATTATA  400
      |||
     351  GAAGCGTTTTGAAAAGAATGGAGTTAAGCATGTCCATGCATTATTATTATA  400
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Fig. 13-2

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401 CTCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
    |||||
401 CTCTACTGGAACGCACTTCTGTGAGGTTGAACAGATAAGGAATGGACCT 450
    |||||
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAAACAACCCA 500
    |||||
451 CCAGTCATTTCATTCTGGAATCAAAGACCTAAAAGTCTTGAAAAACAACCCA 500
    |||||
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
    |||||
501 GTCTGGCTTTGAAGGATTCATCAAGGACCAGTTCACCACCCTCCCTGAGG 550
    |||||
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
    |||||
551 TGAAGGACCGGTGCTTTGCCACCCAAGTGTACTGCAAATGGCGCTACCAC 600
    |||||
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
    |||||
601 CAGGGCAGAGATGTGGACTTTGAGGCCACCTGGGACACTGTTAGGAGCAT 650
    |||||
651 TGTCCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCACCT 700
    |||||
651 TGTCCTGCAGAAATTTGCTGGGCCCTATGACAAAGGCGAGTACTCGCCCT 700
    |||||
701 CTGTGCAGAAGACCCCTCTATGATATCCAGGTGCTCTCCCTGAGCCGAGTT 750
    |||||
701 CTGTCCAGAAGACACTCTATGACATCCAGGTGCTCACCTGGGCCAGGTT 750
    |||||
751 CCTGAGATAGAAGATATGGAATCAGCCTGCCAAACATTCACTACTTCAA 800
    |||||
751 CCTGAGATAGAAGATATGGAATCAGCCTGCCAAATATTCCTACTTTAAA 800
    |||||
801 TATAGACATGTCCAAATGGGTCTGATCAACAAGGAAGAGGTCTTGCTGC 850
    |||||
801 CATAGACATGTCCAAATGGGACTGATCAACAAGGAAGAGGTCTTGCTAC 850
    |||||
851 CATTAGACAATCCATATGGAAAAATTACTGGTACAGTCAAGAGGAAGTTG 900
    |||||
851 CTTTAGACAATCCATATGGCAGGATTACTGGTACAGTCAAGAGGAAGCTG 900
    |||||
901 TCTTCAAGACTGTGA 915
    |||||
901 ACTTCAAGGCTGTGA 915
    |||||

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Fig. 14-1

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"PBC" uricase:

Pig cDNA from 1 to 674 (Apa site) then Baboon cDNA from 675 to 915 (end). PBC chimeric cDNA can be cut out with NcoI plus BamHI

Gap Weight: 50 Average Match: 10.000
Length Weight: 3 Average Mismatch: -9.000

Quality: 7839 Length: 915
Ratio: 8.567 Gaps: 0
Percent Similarity: 92.459 Percent Identity: 92.459

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

PBC.seq x Wubaboon.seq

July 25, 1998 09:36 ..

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PBC      1  ATGGCTCAT|TACCGTAA|TGACTACAAAAA|GAATGATGAGGTAGAGTTTGT  50
          |||||
Bab      1  ATGGCCGACTACCATACA|ACTATAAAAA|GAATGATGAA|TTGGAGTTTGT  50
          |||||
51  CCGAACTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAGCGAG  100
          |||||
51  CCGAACTGGCTATGGGAAGGATATGGTAAAAGTTCTCCATATTCAGCGAG  100
          |||||
101  ATGGAAAAATATCAGCAGCAT|TAAAGAGGTGGCAACTTCAGTGCAACTGACT  150
          |||||
101  ATGGAAAAATATCAGCAGCAT|TAAAGAGGTGGCAACTTCAGTGCAACTTACT  150
          |||||
151  TTGAGCTCCAAAAAAGATTACCTG|CATGGAGACA|AATTCAGATGTGCATCCC  200
          |||||
151  CTGAGTTCCAAAAAAGATTACCTG|CATGGAGATA|AATTCAGATATCATCCC  200
          |||||
201  TACAGACACCATCAAGAACACAGTTAATGT|CCTGGCGAAGTTCAAAGGCA  250
          |||||
201  TACAGACACCATCAAGAACACAGTT|CATGTCT|TGGCAAAGTTTAAAGGAA  250
          |||||
251  TCAAAAGCATAGAAACTTTTGCTGTGACTATCTGTGAGCATTTTCTTTCT  300
          |||||
251  TCAAAAGCATAGAAAGCCTTTGGTGTGAATATTGTGAGTATTTTCTTTCT  300
          |||||
301  TCCTTCAAGCATGTCATCAGAGCTCAAGTCTATGTGGAAGAAGTTCCTTTG  350
          |||||
301  TCTTTTAACCATGTAATCCGAGCTCAAGTCTACGTGGAAGAAATCCCTTTG  350
          |||||
351  GAAGCGTTTGTGAAAAGAAATGGAGTTAAGCATGTCCATGCATTTATTATA  400
          |||||
351  GAAGCGTCTGTGAAAAGAAATGGAGTTAAGCATGTCCATGCATTTATTACA  400
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